

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Baker, Joffre  
Chien, Kenneth  
King, Kathleen  
Pennica, Diane  
Wood, William

10 (ii) TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses  
Therefor

15 (iii) NUMBER OF SEQUENCES: 8

15 (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Genentech, Inc.  
(B) STREET: 460 Point San Bruno Blvd  
(C) CITY: South San Francisco  
20 (D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94080

25 (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: patin (Genentech)

30 (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE: 05-AUG-1994  
(C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/233609  
(B) FILING DATE: 25-APR-1994

40 (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Hasak, Janet E.  
(B) REGISTRATION NUMBER: 28,616  
(C) REFERENCE/DOCKET NUMBER: 894P1

45 (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 415/225-1896  
(B) TELEFAX: 415/952-9881  
(C) TELEX: 910/371-7168

50 (2) INFORMATION FOR SEQ ID NO:1:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1352 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5 GGATAAGCCT GGGGCCAGCA TGAGCCAGAG GGAGGGAAAGT CTGGAAGACC 50  
10 ACCAGACTGA CTCCTCAATC TCATTCCTAC CCCATTTGGA GGCCAAGATC 100  
15 CGCCAGACAC ACAACCTTGC CCGCCTCCTG ACCAAATATG CAGAACAACT 150  
20 TCTGGAGGAA TACGTGCAGC AACAGGGAGA GCCCTTGAGG CTGCCGGGCT 200  
25 TCTCACCACC GCGGCTGCCG CTGGCCGGCC TGAGTGGCCC GGCTCCGAGC 250  
30 CATGCAGGGC TACCGGTGTC CGAGCGGCTG CGGCAGGATG CAGCCGCCCT 300  
35 GAGTGTGCTG CCCGCGCTGT TGGATGCCGT CCGCCGCCGC CAGGCAGGAGC 350  
40 TGAACCCGCG CGCCCCCGCGC CTGCTGCGGA GCCTGGAGGA CGCAGCCCGC 400  
45 CAGGTTCGGG CCCTGGCGC CGCGGTGGAG ACAGTGCTGG CCGCGCTGGG 450  
50 CGCTGCAGCC CGCGGGCCCG GGCCAGAGCC CGTCACCGTC GCCACCCCTCT 500  
55 TCACGGCCAA CAGCACTGCA GGCATCTTCT CAGCCAAGGT GCTGGGGTTC 550  
60 CACGTGTGCG GCCTCTATGG CGAGTGGGTG AGCCGCACAG AGGGCGACCT 600  
65 GGGCCAGCTG GTGCCAGGGG GCGTCGCCTG AGAGTGAATA CTTTTCTTG 650  
70 TAAGCTCGCT CTGTCTCGCC TCTTTGGCTT CAAATTTCT GTCTCTCCAT 700  
75 CTGTGTCCCTG TGTGTTCTTG GGCTGTCCCT ATCTTCTGC ATTTGTGTGG 750  
80 TCTCTCTCTT CTGCTCTCCT CTCTGCAGGG AGCTTCTTTT TTCCAACAGT 800  
85 TTCTCGTTT GTCTCTCTCC AGTCTTGAAC ACTTTGTCT CCGAGAGGTC 850

TCTTTTGTT TCCTTGTCTC TTGGTTCTT CTTGCTTGC TTGCTTGCTT 900

5 GCTTGCTTGT TGTTGAGACA GGGTCTCACC ATATAGCTCT GGATGGCCTG 950

GAACTTGCTA TGTAGGCCAG GCTGGCCTCC AGCTCATAGA GATCCACTTG 1000

10 CCTCCGACTC CCAATTCCC CATCTGTCTC CCTGTGATCC ATATGGGTAT 1050

15 GTGTAACCCT TACTTTGTCT CATGGAGGTG ACAATTTTC TCCCTTCAGT 1100

TTCTTGTTT TTTACTGACC AGAAAAGTGC CTACTTGTCC CCTGGTGGCA 1150

20 AGGCCATTCA CCTTAGGACC TTCCCACCAAG TTCCCTTGTA GGCAAATCCC 1200

25 TCCCCCTTG AGGTCCCTTCC CTTCATACC GCCCTAGGCT GGTCAATGGA 1250

30 GAGAGAAAGG CAGAAAAACA TCTTAAAGA GTTTTATTG AGAATAAATT 1300

35 AATTTTGTA AATAAAATGT TTAACAATAA AACTAAACTT TTATGAAAAA 1350

AA 1352

35 (2) INFORMATION FOR SEQ ID NO:2:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1352 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

50 CCTATTCGGA CCCCGGTCGT ACTCGGTCTC CCTCCCTTCA GACCTTCTGG 50

55 TGGTCTGACT GAGGAGTTAG AGTAAGGATG GGGTAAACCT CCGGTTCTAG 100

60 GCGGTCTGTG TGTTGGAACG GGCAGGAGGAC TGGTTTATAC GTCTTGTGA 150

AGACCTCCTT ATGCACGTCG TTGTCCCTCT CGGGAAACCC GACGGCCCGA 200  
5 AGAGTGGTGG CGCCGACGGC GACCGGCCGG ACTCACCGGG CCGAGGCTCG 250  
GTACGTCCCG ATGGCCACAG GCTCGCCGAC GCCGTCTAC GTCGGCGGGA 300  
10 CTCACACGAC GGGCGCGACA ACCTACGGCA GGCGGCGGCG GTCCGCCTCG 350  
ACTTGGGCCG GCGGGGGCGCG GACGACGCCT CGGACCTCCT GCGTCGGGCG 400  
15 GTCCAAGCCC GGGACCCCGCG GCGCCACCTC TGTACGACCC GGCGCGACCC 450  
GCGACGTCGG GCGCCCGGGC CCGGTCTCGG GCAGTGGCAG CGGTGGGAGA 500  
20 AGTGCCGGTT GTCGTGACGT CCGTAGAAGA GTCGGTTCCA CGACCCCAAG 550  
GTGCACACGC CGGAGATAACC GCTCACCCAC TCGGCGTGTGTC TCCCGCTGGA 600  
25 CCCGGTCGAC CACGGTCCCC CGCAGCGGAC TCTCACTTAT GAAAAAGAAC 650  
ATTCGAGCGA GACAGAGCGG AGAAACCGAA GTTTAAAAGA CAGAGAGGTA 700  
30 GACACAGGAC ACACAAGAAC CCGACAGGGG TAGAAAGACG TAAACACACC 750  
35 AGAGAGAGAA GACGAGAGGA GAGACGTCCC TCGAAGAAAA AAGGTTGTCA 800  
40 AAGAGCAAAA CAGAGAGAGG TCAGAACTTG TGAAAACAGA GGCTCTCCAG 850  
AGAAAAACAA AGGAACAGAG AACCAAGAAA GAAACGAACG AACGAACGAA 900  
45 CGAACGAACA ACAACTCTGT CCCAGAGTGG TATATCGAGA CCTACCGGAC 950  
50 CTTGAACGAT ACATCCGGTC CGACCGGAGG TCGAGTATCT CTAGGTGAAAC 1000  
GGAGGCTGAG GGTTAAAGGG GTAGACAGAG GGACACTAGG TATAACCCATA 1050

CACATTGGGA ATGAAACAGA GTACCTCCAC TGTTAAAAAG AGGGAAGTCA 1100

5 AAGAAACAAG AAATGACTGG TCTTTCACG GATGAACAGG GGACCACCGT 1150

TCCGGTAAGT GGAATCCTGG AAGGGTGGTC AAGGAAACAT CCGTTAGGG 1200

10 AGGGGGAAAC TCCAGGAAGG GAAAGTATGG CGGGATCCGA CCAGTTACCT 1250

CTCTCTTCC GTCTTTGT AGAAATTCT CAAAATAAAC TCTTATTAA 1300

15 TTAAAAACAT TTATTTACA AATTGTTATT TTGATTGAA AATACTTTT 1350

20 TT 1352

25 (2) INFORMATION FOR SEQ ID NO:3:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 203 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

40 Met Ser Gln Arg Glu Gly Ser Leu Glu Asp His Gln Thr Asp Ser  
1 5 10 15

45 Ser Ile Ser Phe Leu Pro His Leu Glu Ala Lys Ile Arg Gln Thr  
20 25 30

50 His Asn Leu Ala Arg Leu Leu Thr Lys Tyr Ala Glu Gln Leu Leu  
35 40 45

55 Glu Glu Tyr Val Gln Gln Gly Glu Pro Phe Gly Leu Pro Gly  
50 55 60

60 Phe Ser Pro Pro Arg Leu Pro Leu Ala Gly Leu Ser Gly Pro Ala  
65 70 75

65 Pro Ser His Ala Gly Leu Pro Val Ser Glu Arg Leu Arg Gln Asp  
80 85 90

70 Ala Ala Ala Leu Ser Val Leu Pro Ala Leu Leu Asp Ala Val Arg  
95 100 105

75 Arg Arg Gln Ala Glu Leu Asn Pro Arg Ala Pro Arg Leu Leu Arg  
110 115 120

Ser Leu Glu Asp Ala Ala Arg Gln Val Arg Ala Leu Gly Ala Ala  
 125 130 135  
 Val Glu Thr Val Leu Ala Ala Leu Gly Ala Ala Ala Arg Gly Pro  
 5 140 145 150  
 Gly Pro Glu Pro Val Thr Val Ala Thr Leu Phe Thr Ala Asn Ser  
 155 160 165  
 Thr Ala Gly Ile Phe Ser Ala Lys Val Leu Gly Phe His Val Cys  
 10 170 175 180  
 Gly Leu Tyr Gly Glu Trp Val Ser Arg Thr Glu Gly Asp Leu Gly  
 185 190 195  
 15 Gln Leu Val Pro Gly Gly Val Ala  
 200 203

20 (2) INFORMATION FOR SEQ ID NO:4:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 200 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Phe Thr Glu His Ser Pro Leu Thr Pro His Arg Arg Asp  
 1 5 10 15  
 Leu Cys Ser Arg Ser Ile Trp Leu Ala Arg Lys Ile Arg Ser Asp  
 35 20 25 30  
 Leu Thr Ala Leu Thr Glu Ser Tyr Val Lys His Gln Gly Leu Asn  
 35 40 45  
 Lys Asn Ile Asn Leu Asp Ser Ala Asp Gly Met Pro Val Ala Ser  
 50 55 60  
 Thr Asp Gln Trp Ser Glu Leu Thr Glu Ala Glu Arg Leu Gln Glu  
 65 70 75  
 Asn Leu Gln Ala Tyr Arg Thr Phe His Val Leu Leu Ala Arg Leu  
 80 85 90  
 45 Leu Glu Asp Gln Gln Val His Phe Thr Pro Thr Glu Gly Asp Phe  
 95 100 105  
 His Gln Ala Ile His Thr Leu Leu Leu Gln Val Ala Ala Phe Ala  
 50 110 115 120  
 Tyr Gln Ile Glu Glu Leu Met Ile Leu Leu Glu Tyr Lys Ile Pro  
 125 130 135

Arg Asn Glu Ala Asp Gly Met Pro Ile Asn Val Gly Asp Gly Gly  
140 145 150

5 Leu Phe Glu Lys Lys Leu Trp Gly Leu Lys Val Leu Gln Glu Leu  
155 160 165

Ser Gln Trp Thr Val Arg Ser Ile His Asp Leu Arg Phe Ile Ser  
170 175 180

10 Ser His Gln Thr Gly Ile Pro Ala Arg Gly Ser His Tyr Ile Ala  
185 190 195

Asn Asn Lys Lys Met  
200

15 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 50 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

30 GC GG CC CG CGA GCT CGA ATT C TTT TTT TTT TTT TTT TTT TTT TTT 50

35 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1018 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GT GA AG GG AG CC GG GG AT CA G CC AG GG GG CC GA GC AT GAG CCG GAG GG AGG GA 50

45 AG TCT GG AAG ACC C C C A G A C T G A T T C C T C A G T C A C T T C T T C C C C A C T T 100

GG AG GG CC AAG AT C C G T C A G A C A C A G G C C T G C G C A C C T C C T C A C C A A T 150

50 ACG CT GAG CA GCT GCT CC AG GA AT AT GT GC AG CT CC AG GG AG AC CC CT TC 200

GGG CT G C C C A G C T T C T C G C C G C G G G C T G C C G G T G G C C G G C G C 250

CCCGGCTCCG AGCCACGCCG GGCTGCCAGT GCACGAGCGG CTGCGGCTGG 300  
5 ACGCGGCCGC GCTGGCCGCG CTGCCCGCG TGCTGGACGC AGTGTGTCGC 350  
CGCCAGGCCG AGCTGAACCC GCGCGGCCG CGCCTGCTGC GCCGCCTGGA 400  
10 GGACGCGCG CGCCAGGCCG GGGCCCTGGG CGCCGCCGTG GAGGCCTTGC 450  
TGGCCGCGCT GGGCGCCGCC AACCGCGGGC CCCGGGCCGA GCCCCCCGCC 500  
15 GCCACCGCCT CAGCCGCCTC CGCCACCGGG GTCTTCCCCG CCAAGGTGCT 550  
GGGGCTCCGC GTTGCGGCC TCTACCGCGA GTGGCTGAGC CGCACCGAGG 600  
20 GCGACCTGGG CCAGCTGCTG CCCGGGGGCT CGGCCTGAGC GCCGCGGGGC 650  
AGCTCGCCCC GCCTCCTCCC GCTGGGTTCC GTCTCTCCTT CCGCTTCTTT 700  
25 GTCTTCTCT GCGCTGTCG GTGTCTGTCT GTCTGCTCTT AGCTGTCTCC 750  
ATTGCCTCGG CCTTCTTGC TTTTGTGGG GGAGAGGGGA GGGGACGGGC 800  
30 AGGGTCTCTG TCGCCCAGGC TGGGGTGCAG TGGCGCGATC CCAGCACTGC 850  
AGCCTCAACC TCCTGGGCTC AAGCCATCCT TCCGCCTCAG CTTCCCCAGC 900  
35 AGCTGGACT ACAGGCACGC GCCACCACAG CCGGCTAATT TTTTATTTAA 950  
40 TTTTTTGTAG AGACGAGGTT TCGCCATGTT GCCCAGGCTG GTCTTGAAC 1000  
45 CCGGGGCTCA AGCGATCC 1018  
50

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1018 bases

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CACTTCCCTC GGCCCTAGTC GGTCCCCGGT CGTACTCGGC CTCCCTCCCT 50  
10 TCAGACCTTC TGGGGGTCTG ACTAAGGAGT CAGAGTGAAG AAGGGGTGAA 100  
15 CCTCCGGTTC TAGGCAGTCT GTGTGTCGGA ACGCGTGGAG GAGTGGTTA 150  
20 TGCAGACTCGT CGACGAGGTC CTTATACACG TCGAGGTCCC TCTGGGAAG 200  
25 CCCGACGGGT CGAAGAGCGG CGGCGCCGAC GGCCACCGGC CGGACTCGCG 250  
30 GGGCCGAGGC TCGGTGCGCC CCGACGGTCA CGTGCTCGCC GACGCCGACC 300  
35 TGCGCCGCCG CGACCGGCGC GACGGGGCG ACGACCTGCG TCACACAGCG 350  
40 GCGGTCCGGC TCGACTTGGG CGCGCGCGC GCGGACGACG CGGGGGACCT 400  
45 CCTGCGCCGC GCGGTCCGGG CCCGGGACCC GCGGCGGCAC CTCCGGAACG 450  
50 ACCGGCGCGA CCCGGCGCGG TTGGCGCCCG GGGCCCGGCT CGGGGGCGG 500  
55 CGGTGGCGGA GTCGGCGGAG GCGGTGGCCC CAGAAGGGGC GGTTCCACGA 550  
60 CCCCCGAGGCG CAAACGCCGG AGATGGCGCT CACCGACTCG GCGTGGCTCC 600  
65 CGCTGGACCC GGTGACGAC GGGCCCCGA GCCGGACTCG CGGCGCCCCG 650  
70 TCGAGCGGGG CGGAGGAGGG CGACCCAAGG CAGAGAGGAA GGCGAAGAAA 700  
75 CAGAAAGAGA CGGCGACAGC CACAGACAGA CAGACGAGAA TCGACAGAGG 750  
80 TAACGGAGCC GGAAGAAACG AAAAACACCC CCTCTCCCT CCCCTGCCCG 800

TCCCCAGAGAC AGCGGGTCCG ACCCCACGTC ACCCGCGCTAG GGTCGTGACG 850

5 TCGGAGTTGG AGGACCCGAG TTCGGTAGGA AGGCAGGAGTC GAAGGGGTCG 900

TCGACCCCTGA TGTCCGTGCG CGGTGGTGTC GGCCGATTAA AAAATAAATT 950

10 AAAAACATC TCTGCTCCAA AGCGGTACAA CGGGTCCGAC CAGAACTTGA 1000

GGCCCCGAGT TCGCTAGG 1018

15

(2) INFORMATION FOR SEQ ID NO:8:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Arg Arg Glu Gly Ser Leu Glu Asp Pro Gln Thr Asp Ser  
1 5 10 15

Ser Val Ser Leu Leu Pro His Leu Glu Ala Lys Ile Arg Gln Thr  
20 25 30

His Ser Leu Ala His Leu Leu Thr Lys Tyr Ala Glu Gln Leu Leu  
35 40 45

Gln Glu Tyr Val Gln Leu Gln Gly Asp Pro Phe Gly Leu Pro Ser  
50 55 60

Phe Ser Pro Pro Arg Leu Pro Val Ala Gly Leu Ser Ala Pro Ala  
65 70 75

40 Pro Ser His Ala Gly Leu Pro Val His Glu Arg Leu Arg Leu Asp  
80 85 90

Ala Ala Ala Leu Ala Ala Leu Pro Pro Leu Leu Asp Ala Val Cys  
95 100 105

Arg Arg Gln Ala Glu Leu Asn Pro Arg Ala Pro Arg Leu Leu Arg  
110 115 120

50 Arg Leu Glu Asp Ala Ala Arg Gln Ala Arg Ala Leu Gly Ala Ala  
125 130 135

Val Glu Ala Leu Leu Ala Ala Leu Gly Ala Ala Asn Arg Gly Pro  
140 145 150

Arg Ala Glu Pro Pro Ala Ala Thr Ala Ser Ala Ala Ser Ala Thr  
155 160 165

5 Gly Val Phe Pro Ala Lys Val Leu Gly Leu Arg Val Cys Gly Leu  
170 175 180

Tyr Arg Glu Trp Leu Ser Arg Thr Glu Gly Asp Leu Gly Gln Leu  
185 190 195

10 Leu Pro Gly Gly Ser Ala  
200 201